SEQUENCE LISTING

<110>   Flannery, Carl R
        Corcoran, Christopher J
        Freeman, Bethany A
        Racie, Lisa A

<120>   RECOMBINANT LUBRICIN MOLECULES AND USES THEREOF

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<151>   2004-08-13

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<151>   2003-08-14

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Thr Thr Ile Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
        370   375   380

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
385   390   395   400

Thr Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
        405   410   415

Thr Lys Pro Ala Pro Thr Thr Pro Glu Thr Pro Pro Pro Thr Thr Ser
        420   425   430

Glu Val Ser Thr Pro Thr Thr Thr Lys Glu Pro Thr Thr Ile His Lys
        435   440   445

Ser Pro Asp Glu Ser Thr Pro Glu Leu Ser Ala Glu Pro Thr Pro Lys
    450   455   460

Ala Leu Glu Asn Ser Pro Lys Glu Pro Gly Val Pro Thr Thr Lys Thr
465   470   475   480

Pro Ala Ala Thr Lys Pro Glu Met Thr Thr Thr Ala Lys Asp Lys Thr
        485   490   495

Thr Glu Arg Asp Leu Arg Thr Thr Pro Glu Thr Thr Thr Ala Ala Pro
        500   505   510

Lys Met Thr Lys Glu Thr Ala Thr Thr Thr Glu Lys Thr Thr Glu Ser
        515   520   525

Lys Ile Thr Ala Thr Thr Thr Gln Val Thr Ser Thr Thr Thr Gln Asp
    530   535   540

Thr Thr Pro Phe Lys Ile Thr Thr Leu Lys Thr Thr Thr Leu Ala Pro
545   550   555   560

Lys Val Thr Thr Thr Lys Lys Thr Ile Thr Thr Thr Glu Ile Met Asn
           565   570   575

Lys Pro Glu Glu Thr Ala Lys Pro Lys Asp Arg Ala Thr Asn Ser Lys

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            580                    585         ·              590

   Ala Thr Thr Pro Lys Pro Gln Lys Pro Thr Lys Ala Pro Lys Lys Pro
           595                 600             605

   Thr Ser Thr Lys Lys Pro Lys Thr Met Pro Arg Val Arg Lys Pro Lys
           610             615             620

   Thr Thr Pro Thr Pro Arg Lys Met Thr Ser Thr Met Pro Glu Leu Asn
   625                 630             635                 640

   Pro Thr Ser Arg Ile Ala Glu Ala Met Leu Gln Thr Thr Thr Arg Pro
               645             650                 655

   Asn Gln Thr Pro Asn Ser Lys Leu Val Glu Val Asn Pro Lys Ser Glu
               660             665             670

   Asp Ala Gly Gly Ala Glu Gly Glu Thr Pro His Met Leu Leu Arg Pro
           675                 680             685

   His Val Phe Met Pro Glu Val Thr Pro Asp Met Asp Tyr Leu Pro Arg
       690                 695             700

   Val Pro Asn Gln Gly Ile Ile Ile Asn Pro Met Leu Ser Asp Glu Thr
   705                 710             715                 720

   Asn Ile Cys Asn Gly Lys Pro Val Asp Gly Leu Thr Thr Leu Arg Asn
                   725             730                 735

   Gly Thr Leu Val Ala Phe Arg Gly His Tyr Phe Trp Met Leu Ser Pro
               740             745             750

   Phe Ser Pro Pro Ser Pro Ala Arg Arg Ile Thr Glu Val Trp Gly Ile
           755             760             765

   Pro Ser Pro Ile Asp Thr Val Phe Thr Arg Cys Asn Cys Glu Gly Lys
       770             775             780

   Thr Phe Phe Phe Lys Asp Ser Gln Tyr Trp Arg Phe Thr Asn Asp Ile
   785             790             795                 800

   Lys Asp Ala Gly Tyr Pro Lys Pro Ile Phe Lys Gly Phe Gly Gly Leu
               805             810             815

   Thr Gly Gln Ile Val Ala Ala Leu Ser Thr Ala Lys Tyr Lys Asn Trp
               820             825             830

   Pro Glu Ser Val Tyr Phe Phe Lys Arg Gly Gly Ser Ile Gln Gln Tyr
           835             840             845

   Ile Tyr Lys Gln Glu Pro Val Gln Lys Cys Pro Gly Arg Arg Pro Ala
       850             855             860

   Leu Asn Tyr Pro Val Tyr Gly Glu Met Thr Gln Val Arg Arg Arg Arg
   865             870             875                 880
```

Phe Glu Arg Ala Ile Gly Pro Ser Gln Thr His Thr Ile Arg Ile Gln
            885   890   895

Tyr Ser Pro Ala Arg Leu Ala Tyr Gln Asp Lys Gly Val Leu His Asn
            900   905   910

Glu Val Lys Val Ser Ile Leu Trp Arg Gly Leu Pro Asn Val Val Thr
      915   920   925

Ser Ala Ile Ser Leu Pro Asn Ile Arg Lys Pro Asp Gly Tyr Asp Tyr
    930   935   940

Tyr Ala Phe Ser Lys Asp Gln Tyr Tyr Asn Ile Asp Val Pro Ser Arg
945   950   955   960

Thr Ala Arg Ala Ile Thr Thr Arg Ser Gly Gln Thr Leu Ser Lys Val
            965   970   975

Trp Tyr Asn Cys Pro
            980

<210> 8
<211> 157
<212> DNA
<213> Artificial

<220>
<223> Lub:1 DNA insert from synthetic cDNA cassette-1.

<400> 8
gcgcgcccac aactccaaaa gagcccgcac ctaccacgac aaagtcagct cctactacgc   60

ccaaagagcc agcgccgacg actactaaag aaccggcacc caccacgcct aaggagccag   120

ctcctactac aacgaaaccg gcaccaacca ctccgga   157

<210> 9
<211> 51
<212> PRT
<213> Artificial

<220>
<223> 51 amino acids encoded by Lub:1 DNA insert (4 KEPAPTT sequences between S373 to E425 in SEQ ID NO: 7).

<400> 9

Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
1   5   10   15

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
            20   25   30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Pro Ala Pro
     35   40   45

Thr Thr Pro
   50

<210> 10
<211> 3024
<212> DNA
<213> Artificial

<220>
<223> Recombinant PRG4-Lub:2 cDNA construct.

<400> 10

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atggcatgga aaacacttcc catttacctg ttgttgctgc tgtctgtttt cgtgattcag      60

caagtttcat ctcaagattt atcaagctgt gcagggagat gtggggaagg gtattctaga     120

gatgccacct gcaactgtga ttataactgt caacactaca tggagtgctg ccctgatttc     180

aagagagtct gcactgcgga gctttcctgt aaaggccgct gctttgagtc cttcgagaga     240

gggagggagt gtgactgcga cgcccaatgt aagaagtatg acaagtgctg tcccgattat     300

gagagtttct gtgcagaagt gcataatccc acatcaccac atcttcaaa gaaagcacct     360

ccaccttcag gagcatctca aaccatcaaa tcaacaacca acgttcacc caaaccacca     420

aacaagaaga agactaagaa agttatagaa tcagaggaaa taacagaaga acattctgtt     480

tctgaaaatc aagagtcctc ctccagtagc agttcaagta gttcgtcgtc gacaatttgg     540

aaaatcaagt cttccaaaaa ttcagctgct aatagagaat tacagaagaa actcaaagta     600

aaagataaca agaagaacag aactaaaaag aaacctaccc ccaaaccacc agttgtagat     660

gaagctggaa gtggattgga caatggtgac ttcaaggtca caactcctga cacgtctacc     720

acccaacaca ataaagtcag cacatctccc aagatcacaa cagcaaaacc aataaatccc     780

agacccagtc ttccacctaa ttctgataca tctaaagaga cgtctttgac agtgaataaa     840

gagacaacag ttgaaactaa agaaactact acaacaaata aacagacttc aactgatgga     900

aaagagaaga ctacttccgc taaagagaca caaagtatag agaaaacatc tgctaaagat     960

ttagcaccca catctaaagt gctggctaaa cctacaccca agctgaaac tacaaccaaa    1020

ggccctgctc tcaccactcc caaggagccc acgcccacca ctcccaagga gcctgcatct    1080

accacaccca aagagcccac acctaccacc atcaagagcg cgcccacaac tccaaaagag    1140
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cccgcaccta ccacgacaaa gtcagctcct actacgccca aagagccagc gccgacgact   1200

actaaagaac cggcacccac cacgcctaaa gaaccagccc ctactacgac aaaggagcct   1260

gcacccacaa ccacgaagag cgcacccaca acaccaaagg agccggcccc tacgactcct   1320

aaggaaccca aaccggcacc aaccactccg gaaacacctc ctccaaccac ttcagaggtc   1380

tctactccaa ctaccaccaa ggagcctacc actatccaca aaagccctga tgaatcaact   1440

cctgagcttt ctgcagaacc cacaccaaaa gctcttgaaa acagtcccaa ggaacctggt   1500

gtacctacaa ctaagacgcc ggcggcgact aaacctgaaa tgactacaac agctaaagac   1560

aagacaacag aaagagactt acgtactaca cctgaaacta caactgctgc acctaagatg   1620

acaaaagaga cagcaactac aacagaaaaa actaccgaat ccaaaataac agctacaacc   1680

acacaagtaa catctaccac aactcaagat accacaccat tcaaaattac tactcttaaa   1740

acaactactc ttgcacccaa agtaactaca acaaaaaaga caattactac cactgagatt   1800

atgaacaaac ctgaagaaac agctaaacca aaagacagag ctactaattc taaagcgaca   1860

actcctaaac ctcaaaagcc aaccaaagca cccaaaaaac ccacttctac caaaaagcca   1920

aaaacaatgc ctagagtgag aaaaccaaag acgacaccaa ctccccgcaa gatgacatca   1980

acaatgccag aattgaaccc tacctcaaga atagcagaag ccatgctcca aaccaccacc   2040

agacctaacc aaactccaaa ctccaaacta gttgaagtaa atccaaagag tgaagatgca   2100

ggtggtgctg aaggagaaac acctcatatg cttctcaggc cccatgtgtt catgcctgaa   2160

gttactcccg acatggatta cttaccgaga gtacccaatc aaggcattat catcaatccc   2220

atgctttccg atgagaccaa tatatgcaat ggtaagccag tagatggact gactactttg   2280

cgcaatggga cattagttgc attccgaggt cattatttct ggatgctaag tccattcagt   2340

ccaccatctc cagctcgcag aattactgaa gtttggggta ttccttcccc cattgatact   2400

gttttactta ggtgcaactg tgaaggaaaa actttcttct ttaaggattc tcagtactgg   2460

cgttttacca atgatataaa agatgcaggg taccccaaac caattttcaa aggatttgga   2520

ggactaactg gacaaatagt ggcagcgctt tcaacagcta aatataagaa ctggcctgaa   2580

tctgtgtatt ttttcaagag aggtggcagc attcagcagt atatttataa acaggaacct   2640

gtacagaagt gccctggaag aaggcctgct ctaaattatc cagtgtatgg agaaatgaca   2700

caggttagga gacgtcgctt tgaacgtgct ataggacctt ctcaaacaca caccatcaga   2760

attcaatatt cacctgccag actggcttat caagacaaag gtgtccttca taatgaagtt   2820
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aaagtgagta tactgtggag aggacttcca aatgtggtta cctcagctat atcactgccc   2880

aacatcagaa aacctgacgg ctatgattac tatgcctttt ctaaagatca atactataac   2940

attgatgtgc ctagtagaac agcaagagca attactactc gttctgggca gaccttatcc   3000

aaagtctggt acaactgtcc ttaa   3024

<210> 11
<211> 1007
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of entire PRG4-LUB:2 protein.

<400> 11

Met Ala Trp Lys Thr Leu Pro Ile Tyr Leu Leu Leu Leu Leu Ser Val
1   5   10   15

Phe Val Ile Gln Gln Val Ser Ser Gln Asp Leu Ser Ser Cys Ala Gly
            20   25   30

Arg Cys Gly Glu Gly Tyr Ser Arg Asp Ala Thr Cys Asn Cys Asp Tyr
            35   40   45

Asn Cys Gln His Tyr Met Glu Cys Cys Pro Asp Phe Lys Arg Val Cys
        50   55   60

Thr Ala Glu Leu Ser Cys Lys Gly Arg Cys Phe Glu Ser Phe Glu Arg
65   70   75   80

Gly Arg Glu Cys Asp Cys Asp Ala Gln Cys Lys Lys Tyr Asp Lys Cys
                85   90   95

Cys Pro Asp Tyr Glu Ser Phe Cys Ala Glu Val His Asn Pro Thr Ser
            100   105   110

Pro Pro Ser Ser Lys Lys Ala Pro Pro Pro Ser Gly Ala Ser Gln Thr
            115   120   125

Ile Lys Ser Thr Thr Lys Arg Ser Pro Lys Pro Pro Asn Lys Lys Lys
        130   135   140

Thr Lys Lys Val Ile Glu Ser Glu Glu Ile Thr Glu Glu His Ser Val
145   150   155   160

Ser Glu Asn Gln Glu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
            165   170   175

Ser Thr Ile Trp Lys Ile Lys Ser Ser Lys Asn Ser Ala Ala Asn Arg
            180   185   190

Glu Leu Gln Lys Lys Leu Lys Val Lys Asp Asn Lys Lys Asn Arg Thr
       195   200   205

Lys Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu Ala Gly Ser
   210   215   220

Gly Leu Asp Asn Gly Asp Phe Lys Val Thr Thr Pro Asp Thr Ser Thr
225   230   235   240

Thr Gln His Asn Lys Val Ser Thr Ser Pro Lys Ile Thr Thr Ala Lys
          245   250   255

Pro Ile Asn Pro Arg Pro Ser Leu Pro Pro Asn Ser Asp Thr Ser Lys
         260   265   270

Glu Thr Ser Leu Thr Val Asn Lys Glu Thr Thr Val Glu Thr Lys Glu
     275   280   285

Thr Thr Thr Thr Asn Lys Gln Thr Ser Thr Asp Gly Lys Glu Lys Thr
   290   295   300

Thr Ser Ala Lys Glu Thr Gln Ser Ile Glu Lys Thr Ser Ala Lys Asp
305   310   315   320

Leu Ala Pro Thr Ser Lys Val Leu Ala Lys Pro Thr Pro Lys Ala Glu
         325   330   335

Thr Thr Thr Lys Gly Pro Ala Leu Thr Thr Pro Lys Glu Pro Thr Pro
       340   345   350

Thr Thr Pro Lys Glu Pro Ala Ser Thr Thr Pro Lys Glu Pro Thr Pro
   355   360   365

Thr Thr Ile Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
   370   375   380

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
385   390   395   400

Thr Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
         405   410   415

Thr Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro
         420   425   430

Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr
         435   440   445

Thr Pro Glu Thr Pro Pro Pro Thr Thr Ser Glu Val Ser Thr Pro Thr
   450   455   460

Thr Thr Lys Glu Pro Thr Thr Ile His Lys Ser Pro Asp Glu Ser Thr
465   470   475   480

Pro Glu Leu Ser Ala Glu Pro Thr Pro Lys Ala Leu Glu Asn Ser Pro
           485   490   495

Lys Glu Pro Gly Val Pro Thr Thr Lys Thr Pro Ala Ala Thr Lys Pro
         500   505   510

Glu Met Thr Thr Thr Ala Lys Asp Lys Thr Thr Glu Arg Asp Leu Arg
        515   520   525

Thr Thr Pro Glu Thr Thr Thr Ala Ala Pro Lys Met Thr Lys Glu Thr
    530   535   540

Ala Thr Thr Thr Glu Lys Thr Thr Glu Ser Lys Ile Thr Ala Thr Thr
545   550   555   560

Thr Gln Val Thr Ser Thr Thr Thr Gln Asp Thr Thr Pro Phe Lys Ile
            565   570   575

Thr Thr Leu Lys Thr Thr Thr Leu Ala Pro Lys Val Thr Thr Thr Lys
        580   585   590

Lys Thr Ile Thr Thr Thr Glu Ile Met Asn Lys Pro Glu Glu Thr Ala
        595   600   605

Lys Pro Lys Asp Arg Ala Thr Asn Ser Lys Ala Thr Thr Pro Lys Pro
    610   615   620

Gln Lys Pro Thr Lys Ala Pro Lys Lys Pro Thr Ser Thr Lys Lys Pro
625   630   · 635   640

Lys Thr Met Pro Arg Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg
        645   650   655

Lys Met Thr Ser Thr Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala
        660   665   670

Glu Ala Met Leu Gln Thr Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser
        675   680   685

Lys Leu Val Glu Val Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu
    690   695   700

Gly Glu Thr Pro His Met Leu Leu Arg Pro His Val Phe Met Pro Glu
705   710   715   720

Val Thr Pro Asp Met Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile
        725   730   735

Ile Ile Asn Pro Met Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys
        740   745   750

Pro Val Asp Gly Leu Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe
        755   760   765

Arg Gly His Tyr Phe Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro

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           770                    775                    780

Ala Arg Arg Ile Thr Glu Val Trp Gly Ile Pro Ser Pro Ile Asp Thr
785             790             795                 800

Val Phe Thr Arg Cys Asn Cys Glu Gly Lys Thr Phe Phe Phe Lys Asp
            805             810             815

Ser Gln Tyr Trp Arg Phe Thr Asn Asp Ile Lys Asp Ala Gly Tyr Pro
            820             825             830

Lys Pro Ile Phe Lys Gly Phe Gly Gly Leu Thr Gly Gln Ile Val Ala
        835             840             845

Ala Leu Ser Thr Ala Lys Tyr Lys Asn Trp Pro Glu Ser Val Tyr Phe
        850             855             860

Phe Lys Arg Gly Gly Ser Ile Gln Gln Tyr Ile Tyr Lys Gln Glu Pro
865             870             875             880

Val Gln Lys Cys Pro Gly Arg Arg Pro Ala Leu Asn Tyr Pro Val Tyr
            885             890             895

Gly Glu Met Thr Gln Val Arg Arg Arg Arg Phe Glu Arg Ala Ile Gly
            900             905             910

Pro Ser Gln Thr His Thr Ile Arg Ile Gln Tyr Ser Pro Ala Arg Leu
        915             920             925

Ala Tyr Gln Asp Lys Gly Val Leu His Asn Glu Val Lys Val Ser Ile
        930             935             940

Leu Trp Arg Gly Leu Pro Asn Val Val Thr Ser Ala Ile Ser Leu Pro
945             950             955             960

Asn Ile Arg Lys Pro Asp Gly Tyr Asp Tyr Tyr Ala Phe Ser Lys Asp
            965             970             975

Gln Tyr Tyr Asn Ile Asp Val Pro Ser Arg Thr Ala Arg Ala Ile Thr
            980             985             990

Thr Arg Ser Gly Gln Thr Leu Ser  Lys Val Trp Tyr Asn  Cys Pro
        995             1000            1005
```

```
<210>  12
<211>  235
<212>  DNA
<213>  Artificial

<220>
<223>  Lub:2 DNA insert from synthetic cDNA cassette-1 and one synthetic
       cDNA cassette-2 sequence.

<400>  12
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gcgcgcccac aactccaaaa gagcccgcac ctaccacgac aaagtcagct cctactacgc      60

ccaaagagcc agcgccgacg actactaaag aaccggcacc caccacgcct aaagaaccag     120

cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgcaccc acaacaccaa     180

aggagccggc ccctacgact cctaaggaac ccaaaccggc accaaccact ccgga         235
```

```
<210>  13
<211>  77
<212>  PRT
<213>  Artificial

<220>
<223>  77 amino acids encoded by Lub:2 DNA insert (6 KEPAPTT sequences
       between S373 and E451 in SEQ ID NO: 11).

<400>  13
```

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Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
1               5                   10             15

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
            20                  25                  30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
        35                  40                  45

Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro
    50                  55                  60

Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro
65                  70                  75
```

```
<210>  14
<211>  3117
<212>  DNA
<213>  Artificial

<220>
<223>  Recombinant PRG4-Lub:3 cDNA construct.

<400>  14
atggcatgga aaacacttcc catttacctg ttgttgctgc tgtctgtttt cgtgattcag      60

caagtttcat ctcaagattt atcaagctgt gcagggagat gtggggaagg gtattctaga     120

gatgccacct gcaactgtga ttataactgt caacactaca tggagtgctg ccctgatttc     180

aagagagtct gcactgcgga gctttcctgt aaaggccgct gctttgagtc cttcgagaga     240

gggagggagt gtgactgcga cgcccaatgt aagaagtatg acaagtgctg tcccgattat     300
```

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gagagtttct gtgcagaagt gcataatccc acatcaccac catcttcaaa gaaagcacct    360

ccaccttcag gagcatctca aaccatcaaa tcaacaacca aacgttcacc caaaccacca    420

aacaagaaga agactaagaa agttatagaa tcagaggaaa taacagaaga acattctgtt    480

tctgaaaatc aagagtcctc ctccagtagc agttcaagta gttcgtcgtc gacaatttgg    540

aaaatcaagt cttccaaaaa ttcagctgct aatagagaat tacagaagaa actcaaagta    600

aaagataaca agaagaacag aactaaaaag aaacctaccc ccaaaccacc agttgtagat    660

gaagctggaa gtggattgga caatggtgac ttcaaggtca caactcctga cacgtctacc    720

acccaacaca ataaagtcag cacatctccc aagatcacaa cagcaaaacc aataaatccc    780

agacccagtc ttccacctaa ttctgataca tctaaagaga cgtctttgac agtgaataaa    840

gagacaacag ttgaaactaa agaaactact acaacaaata aacagacttc aactgatgga    900

aaagagaaga ctacttccgc taaagagaca caaagtatag agaaaacatc tgctaaagat    960

ttagcaccca catctaaagt gctggctaaa cctacaccca aagctgaaac tacaaccaaa   1020

ggccctgctc tcaccactcc caaggagccc acgcccacca ctcccaagga gcctgcatct   1080

accacaccca aagagcccac acctaccacc atcaagagcg cgcccacaac tccaaaagag   1140

cccgcaccta ccacgacaaa gtcagctcct actacgccca aagagccagc gccgacgact   1200

actaaagaac cggcacccac cacgcctaaa gaaccagccc ctactacgac aaaggagcct   1260

gcacccacaa ccacgaagag cgcacccaca acaccaaagg agccggcccc tacgactcct   1320

aaagaaccag cccctactac gacaaaggag cctgcacccca caaccacgaa gagcgcaccc   1380

acaacaccaa aggagccggc ccctacgact cctaaggaac ccaaaccggc accaaccact   1440

ccggaaacac ctcctccaac cacttcagag gtctctactc caactaccac caaggagcct   1500

accactatcc acaaaagccc tgatgaatca actcctgagc tttctgcaga acccacacca   1560

aaagctcttg aaaacagtcc caaggaacct ggtgtaccta caactaagac gccggcggcg   1620

actaaacctg aaatgactac aacagctaaa gacaagacaa cagaaagaga cttacgtact   1680

acacctgaaa ctacaactgc tgcacctaag atgacaaaag agacagcaac tacaacagaa   1740

aaaactaccg aatccaaaat aacagctaca accacacaag taacatctac cacaactcaa   1800

gataccacac cattcaaaat tactactctt aaaacaacta ctcttgcacc caaagtaact   1860

acaacaaaaa agacaattac taccactgag attatgaaca aacctgaaga aacagctaaa   1920

ccaaaagaca gagctactaa ttctaaagcg acaactccta aacctcaaaa gccaaccaaa   1980
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```
gcacccaaaa aacccacttc taccaaaaag ccaaaaacaa tgcctagagt gagaaaacca   2040

aagacgacac caactccccg caagatgaca tcaacaatgc cagaattgaa ccctacctca   2100

agaatagcag aagccatgct ccaaaccacc accagaccta accaaactcc aaactccaaa   2160

ctagttgaag taaatccaaa gagtgaagat gcaggtggtg ctgaaggaga aacacctcat   2220

atgcttctca ggccccatgt gttcatgcct gaagttactc ccgacatgga ttacttaccg   2280

agagtaccca atcaaggcat tatcatcaat cccatgcttt ccgatgagac caatatatgc   2340

aatggtaagc cagtagatgg actgactact ttgcgcaatg ggacattagt tgcattccga   2400

ggtcattatt tctggatgct aagtccattc agtccaccat ctccagctcg cagaattact   2460

gaagtttggg gtattccttc ccccattgat actgttttta ctaggtgcaa ctgtgaagga   2520

aaaactttct tctttaagga ttctcagtac tggcgtttta ccaatgatat aaaagatgca   2580

gggtacccca aaccaatttt caaaggattt ggaggactaa ctggacaaat agtggcagcg   2640

ctttcaacag ctaaatataa gaactggcct gaatctgtgt attttttcaa gagaggtggc   2700

agcattcagc agtatattta taaacaggaa cctgtacaga agtgccctgg aagaaggcct   2760

gctctaaatt atccagtgta tggagaaatg acacaggtta ggagacgtcg ctttgaacgt   2820

gctataggac cttctcaaac acacaccatc agaattcaat attcacctgc cagactggct   2880

tatcaagaca aaggtgtcct tcataatgaa gttaaagtga gtatactgtg gagaggactt   2940

ccaaatgtgg ttacctcagc tatatcactg cccaacatca gaaacctga cggctatgat    3000

tactatgcct tttctaaaga tcaatactat aacattgatg tgcctagtag aacagcaaga   3060

gcaattacta ctcgttctgg cagaccctta tccaaagtct ggtacaactg tccttaa      3117
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<210>  15
<211>  1038
<212>  PRT
<213>  Artificial

<220>
<223>  amino acid sequence of entire PRG4-LUB:3 protein

<400>  15

Met Ala Trp Lys Thr Leu Pro Ile Tyr Leu Leu Leu Leu Ser Val
1               5                   10                  15

Phe Val Ile Gln Gln Val Ser Ser Gln Asp Leu Ser Ser Cys Ala Gly
            20                  25                  30
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```
Arg Cys Gly Glu Gly Tyr Ser Arg Asp Ala Thr Cys Asn Cys Asp Tyr
        35              40              45

Asn Cys Gln His Tyr Met Glu Cys Cys Pro Asp Phe Lys Arg Val Cys
    50              55              60

Thr Ala Glu Leu Ser Cys Lys Gly Arg Cys Phe Glu Ser Phe Glu Arg
65              70              75              80

Gly Arg Glu Cys Asp Cys Asp Ala Gln Cys Lys Lys Tyr Asp Lys Cys
            85              90              95

Cys Pro Asp Tyr Glu Ser Phe Cys Ala Glu Val His Asn Pro Thr Ser
            100             105             110

Pro Pro Ser Ser Lys Lys Ala Pro Pro Pro Ser Gly Ala Ser Gln Thr
        115             120             125

Ile Lys Ser Thr Thr Lys Arg Ser Pro Lys Pro Pro Asn Lys Lys Lys
    130             135             140

Thr Lys Lys Val Ile Glu Ser Glu Glu Ile Thr Glu Glu His Ser Val
145             150             155             160

Ser Glu Asn Gln Glu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
            165             170             175

Ser Thr Ile Trp Lys Ile Lys Ser Ser Lys Asn Ser Ala Ala Asn Arg
            180             185             190

Glu Leu Gln Lys Lys Leu Lys Val Lys Asp Asn Lys Lys Asn Arg Thr
        195             200             205

Lys Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu Ala Gly Ser
    210             215             220

Gly Leu Asp Asn Gly Asp Phe Lys Val Thr Thr Pro Asp Thr Ser Thr
225             230             235             240

Thr Gln His Asn Lys Val Ser Thr Ser Pro Lys Ile Thr Thr Ala Lys
            245             250             255

Pro Ile Asn Pro Arg Pro Ser Leu Pro Pro Asn Ser Asp Thr Ser Lys
            260             265             270

Glu Thr Ser Leu Thr Val Asn Lys Glu Thr Thr Val Glu Thr Lys Glu
        275             280             285

Thr Thr Thr Thr Asn Lys Gln Thr Ser Thr Asp Gly Lys Glu Lys Thr
    290             295             300

Thr Ser Ala Lys Glu Thr Gln Ser Ile Glu Lys Thr Ser Ala Lys Asp
305             310             315             320
```

Leu Ala Pro Thr Ser Lys Val Leu Ala Lys Pro Thr Pro Lys Ala Glu
            325   330   335

Thr Thr Thr Lys Gly Pro Ala Leu Thr Thr Pro Lys Glu Pro Thr Pro
            340   345   350

Thr Thr Pro Lys Glu Pro Ala Ser Thr Thr Pro Lys Glu Pro Thr Pro
            355   360   365

Thr Thr Ile Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
    370   375   380

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
385   390   395   400

Thr Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
            405   410   415

Thr Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro
            420   425   430

Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr
            435   440   445

Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys
    450   455   460

Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr
465   470   475   480

Pro Glu Thr Pro Pro Pro Thr Thr Ser Glu Val Ser Thr Pro Thr Thr
            485   490   495

Thr Lys Glu Pro Thr Thr Ile His Lys Ser Pro Asp Glu Ser Thr Pro
            500   505   510

Glu Leu Ser Ala Glu Pro Thr Pro Lys Ala Leu Glu Asn Ser Pro Lys
    515   520   525

Glu Pro Gly Val Pro Thr Thr Lys Thr Pro Ala Ala Thr Lys Pro Glu
    530   535   540

Met Thr Thr Thr Ala Lys Asp Lys Thr Thr Glu Arg Asp Leu Arg Thr
545   550   555   560

Thr Pro Glu Thr Thr Thr Ala Ala Pro Lys Met Thr Lys Glu Thr Ala
            565   570   575

Thr Thr Thr Glu Lys Thr Thr Glu Ser Lys Ile Thr Ala Thr Thr Thr
            580   585   590

Gln Val Thr Ser Thr Thr Thr Gln Asp Thr Thr Pro Phe Lys Ile Thr
    595   600   605

Thr Leu Lys Thr Thr Thr Leu Ala Pro Lys Val Thr Thr Thr Lys Lys

```
            610                    615                    620
Thr Ile Thr Thr Thr Glu Ile Met Asn Lys Pro Glu Glu Thr Ala Lys
625             630             635             640

Pro Lys Asp Arg Ala Thr Asn Ser Lys Ala Thr Thr Pro Lys Pro Gln
            645             650             655

Lys Pro Thr Lys Ala Pro Lys Lys Pro Thr Ser Thr Lys Lys Pro Lys
        660             665             670

Thr Met Pro Arg Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg Lys
        675             680             685

Met Thr Ser Thr Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala Glu
        690             695             700

Ala Met Leu Gln Thr Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser Lys
705             710             715             720

Leu Val Glu Val Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu Gly
            725             730             735

Glu Thr Pro His Met Leu Leu Arg Pro His Val Phe Met Pro Glu Val
            740             745             750

Thr Pro Asp Met Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile Ile
            755             760             765

Ile Asn Pro Met Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys Pro
            770             775             780

Val Asp Gly Leu Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe Arg
785             790             795             800

Gly His Tyr Phe Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro Ala
            805             810             815

Arg Arg Ile Thr Glu Val Trp Gly Ile Pro Ser Pro Ile Asp Thr Val
            820             825             830

Phe Thr Arg Cys Asn Cys Glu Gly Lys Thr Phe Phe Phe Lys Asp Ser
        835             840             845

Gln Tyr Trp Arg Phe Thr Asn Asp Ile Lys Asp Ala Gly Tyr Pro Lys
    850             855             860

Pro Ile Phe Lys Gly Phe Gly Gly Leu Thr Gly Gln Ile Val Ala Ala
865             870             875             880

Leu Ser Thr Ala Lys Tyr Lys Asn Trp Pro Glu Ser Val Tyr Phe Phe
            885             890             895

Lys Arg Gly Gly Ser Ile Gln Gln Tyr Ile Tyr Lys Gln Glu Pro Val
            900             905             910
```

```
Gln Lys Cys Pro Gly Arg Arg Pro Ala Leu Asn Tyr Pro Val Tyr Gly
        915             920             925

Glu Met Thr Gln Val Arg Arg Arg Arg Phe Glu Arg Ala Ile Gly Pro
    930             935             940

Ser Gln Thr His Thr Ile Arg Ile Gln Tyr Ser Pro Ala Arg Leu Ala
945             950             955             960

Tyr Gln Asp Lys Gly Val Leu His Asn Glu Val Lys Val Ser Ile Leu
            965             970             975

Trp Arg Gly Leu Pro Asn Val Val Thr Ser Ala Ile Ser Leu Pro Asn
            980             985             990

Ile Arg Lys Pro Asp Gly Tyr Asp  Tyr Tyr Ala Phe Ser  Lys Asp Gln
        995             1000             1005

Tyr Tyr  Asn Ile Asp Val Pro  Ser Arg Thr Ala Arg  Ala Ile Thr
    1010             1015             1020

Thr Arg  Ser Gly Gln Thr Leu  Ser Lys Val Trp Tyr  Asn Cys Pro
    1025             1030             1035
```

```
<210>  16
<211>  328
<212>  DNA
<213>  Artificial

<220>
<223>  Lub:3 DNA insert from synthetic cDNA cassette-1 and two synthetic
       cDNA cassette-2 sequences.

<400>  16
gcgcgcccac aactccaaaa gagcccgcac ctaccacgac aaagtcagct cctactacgc      60

ccaaagagcc agcgccgacg actactaaag aaccggcacc caccacgcct aaagaaccag     120

cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgcaccc acaacaccaa     180

aggagccggc ccctacgact cctaaagaac cagcccctac tacgacaaag gagcctgcac     240

ccacaaccac gaagagcgca cccacaacac caaaggagcc ggcccctacg actcctaagg     300

aacccaaacc ggcaccaacc actccgga                                        328
```

```
<210>  17
<211>  108
<212>  PRT
<213>  Artificial

<220>
```

<223> 108 amino acids encoded by Lub:3 DNA insert (9 KEPAPTT sequences
      between S373 and E482 in SEQ ID NO: 15)

<400> 17

Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
1   5   10   15

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
          20   25   30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
          35   40   45

Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro
      50   55   60

Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro
65   70   75   80

Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
              85   90   95

Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro
          100   105

<210> 18
<211> 3210
<212> DNA
<213> Artificial

<220>
<223> recombinant PRG4-Lub:4 cDNA construct.

<400> 18
atggcatgga aaacacttcc catttacctg ttgttgctgc tgtctgtttt cgtgattcag   60

caagtttcat ctcaagattt atcaagctgt gcagggagat gtggggaagg gtattctaga   120

gatgccacct gcaactgtga ttataactgt caacactaca tggagtgctg ccctgatttc   180

aagagagtct gcactgcgga gctttcctgt aaaggccgct gctttgagtc cttcgagaga   240

gggagggagt gtgactgcga cgcccaatgt aagaagtatg acaagtgctg tcccgattat   300

gagagtttct gtgcagaagt gcataatccc acatcaccac catcttcaaa gaaagcacct   360

ccaccttcag gagcatctca aaccatcaaa tcaacaacca aacgttcacc caaaccacca   420

aacaagaaga agactaagaa agttatagaa tcagaggaaa taacagaaga acattctgtt   480

tctgaaaatc aagagtcctc ctccagtagc agttcaagta gttcgtcgtc gacaatttgg   540

aaaatcaagt cttccaaaaa ttcagctgct aatagagaat tacagaagaa actcaaagta   600

```
aaagataaca agaagaacag aactaaaaag aaacctaccc ccaaaccacc agttgtagat    660

gaagctggaa gtggattgga caatggtgac ttcaaggtca caactcctga cacgtctacc    720

acccaacaca ataaagtcag cacatctccc aagatcacaa cagcaaaacc aataaatccc    780

agacccagtc ttccacctaa ttctgataca tctaaagaga cgtctttgac agtgaataaa    840

gagacaacag ttgaaactaa agaaactact acaacaaata aacagacttc aactgatgga    900

aaagagaaga ctacttccgc taaagagaca caaagtatag agaaaacatc tgctaaagat    960

ttagcaccca catctaaagt gctggctaaa cctacaccca aagctgaaac tacaaccaaa   1020

ggccctgctc tcaccactcc caaggagccc acgcccacca ctcccaagga gcctgcatct   1080

accacaccca aagagcccac acctaccacc atcaagagcg cgcccacaac tccaaaagag   1140

cccgcaccta ccacgacaaa gtcagctcct actacgccca aagagccagc gccgacgact   1200

actaaagaac cggcacccac cacgcctaaa gaaccagccc ctactacgac aaaggagcct   1260

gcacccacaa ccacgaagag cgcacccaca acaccaaagg agccggcccc tacgactcct   1320

aaagaaccag cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgcaccc   1380

acaacaccaa aggagccggc ccctacgact cctaaagaac cagcccctac tacgacaaag   1440

gagcctgcac ccacaaccac gaagagcgca cccacaacac caaaggagcc ggcccctacg   1500

actcctaagg aacccaaacc ggcaccaacc actccggaaa cacctcctcc aaccacttca   1560

gaggtctcta ctccaactac caccaaggag cctaccacta tccacaaaag ccctgatgaa   1620

tcaactcctg agctttctgc agaacccaca ccaaaagctc ttgaaaacag tcccaaggaa   1680

cctggtgtac ctacaactaa gacgccggcg gcgactaaac ctgaaatgac tacaacagct   1740

aaagacaaga caacagaaag agacttacgt actacacctg aaactacaac tgctgcacct   1800

aagatgacaa aagagacagc aactacaaca gaaaaaacta ccgaatccaa ataacagct   1860

acaaccacac aagtaacatc taccacaact caagatacca caccattcaa aattactact   1920

cttaaaacaa ctactcttgc acccaaagta actacaacaa aaaagacaat tactaccact   1980

gagattatga caaacctga agaaacagct aaaccaaaag acagagctac taattctaaa    2040

gcgacaactc ctaaacctca aaagccaacc aaagcaccca aaaaacccac ttctaccaaa    2100

aagccaaaaa caatgcctag agtgagaaaa ccaaagacga caccaactcc ccgcaagatg    2160

acatcaacaa tgccagaatt gaaccctacc tcaagaatag cagaagccat gctccaaacc    2220
```

```
accaccagac ctaaccaaac tccaaactcc aaactagttg aagtaaatcc aaagagtgaa    2280

gatgcaggtg gtgctgaagg agaaacacct catatgcttc tcaggcccca tgtgttcatg    2340

cctgaagtta ctcccgacat ggattactta ccgagagtac ccaatcaagg cattatcatc    2400

aatcccatgc tttccgatga gaccaatata tgcaatggta agccagtaga tggactgact    2460

actttgcgca atgggacatt agttgcattc cgaggtcatt atttctggat gctaagtcca    2520

ttcagtccac catctccagc tcgcagaatt actgaagttt ggggtattcc ttcccccatt    2580

gatactgttt ttactaggtg caactgtgaa ggaaaaactt tcttctttaa ggattctcag    2640

tactggcgtt ttaccaatga tataaaagat gcagggtacc ccaaaccaat tttcaaagga    2700

tttggaggac taactggaca aatagtggca gcgctttcaa cagctaaata taagaactgg    2760

cctgaatctg tgtattttt caagagaggt ggcagcattc agcagtatat ttataaacag    2820

gaacctgtac agaagtgccc tggaagaagg cctgctctaa attatccagt gtatggagaa    2880

atgacacagg ttaggagacg tcgctttgaa cgtgctatag gaccttctca aacacacacc    2940

atcagaattc aatattcacc tgccagactg gcttatcaag acaaaggtgt ccttcataat    3000

gaagttaaag tgagtatact gtggagagga cttccaaatg tggttacctc agctatatca    3060

ctgcccaaca tcagaaaacc tgacggctat gattactatg ccttttctaa agatcaatac    3120

tataacattg atgtgcctag tagaacagca agagcaatta ctactcgttc tgggcagacc    3180

ttatccaaag tctggtacaa ctgtccttaa                                    3210
```

<210> 19
<211> 1069
<212> PRT
<213> Artificial

<220>
<223> amino acid sequence of entire PRG4-LUB:4 protein.

<400> 19

```
Met Ala Trp Lys Thr Leu Pro Ile Tyr Leu Leu Leu Leu Leu Ser Val
1               5                  10                  15

Phe Val Ile Gln Gln Val Ser Ser Gln Asp Leu Ser Ser Cys Ala Gly
            20                  25                  30

Arg Cys Gly Glu Gly Tyr Ser Arg Asp Ala Thr Cys Asn Cys Asp Tyr
        35                  40                  45

Asn Cys Gln His Tyr Met Glu Cys Cys Pro Asp Phe Lys Arg Val Cys
```

```
            50                    55                    60

Thr Ala Glu Leu Ser Cys Lys Gly Arg Cys Phe Glu Ser Phe Glu Arg
65                  70                  75                  80

Gly Arg Glu Cys Asp Cys Asp Ala Gln Cys Lys Lys Tyr Asp Lys Cys
                85                  90                  95

Cys Pro Asp Tyr Glu Ser Phe Cys Ala Glu Val His Asn Pro Thr Ser
                100                 105                 110

Pro Pro Ser Ser Lys Lys Ala Pro Pro Pro Ser Gly Ala Ser Gln Thr
        115                 120                 125

Ile Lys Ser Thr Thr Lys Arg Ser Pro Lys Pro Pro Asn Lys Lys Lys
    130                 135                 140

Thr Lys Lys Val Ile Glu Ser Glu Glu Ile Thr Glu Glu His Ser Val
145                 150                 155                 160

Ser Glu Asn Gln Glu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
                165                 170                 175

Ser Thr Ile Trp Lys Ile Lys Ser Ser Lys Asn Ser Ala Ala Asn Arg
            180                 185                 190

Glu Leu Gln Lys Lys Leu Lys Val Lys Asp Asn Lys Lys Asn Arg Thr
        195                 200                 205

Lys Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu Ala Gly Ser
    210                 215                 220

Gly Leu Asp Asn Gly Asp Phe Lys Val Thr Thr Pro Asp Thr Ser Thr
225                 230                 235                 240

Thr Gln His Asn Lys Val Ser Thr Ser Pro Lys Ile Thr Thr Ala Lys
            245                 250                 255

Pro Ile Asn Pro Arg Pro Ser Leu Pro Pro Asn Ser Asp Thr Ser Lys
            260                 265                 270

Glu Thr Ser Leu Thr Val Asn Lys Glu Thr Thr Val Glu Thr Lys Glu
        275                 280                 285

Thr Thr Thr Thr Asn Lys Gln Thr Ser Thr Asp Gly Lys Glu Lys Thr
    290                 295                 300

Thr Ser Ala Lys Glu Thr Gln Ser Ile Glu Lys Thr Ser Ala Lys Asp
305                 310                 315                 320

Leu Ala Pro Thr Ser Lys Val Leu Ala Lys Pro Thr Pro Lys Ala Glu
            325                 330                 335

Thr Thr Thr Lys Gly Pro Ala Leu Thr Thr Pro Lys Glu Pro Thr Pro
        340                 345                 350
```

Thr Thr Pro Lys Glu Pro Ala Ser Thr Thr Pro Lys Glu Pro Thr Pro
        355   360   365

Thr Thr Ile Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
        370   375   380

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
385   390   395   400

Thr Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
            405   410   415

Thr Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro
            420   425   430

Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr
        435   440   445

Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys
        450   455   460

Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys
465   470   · 475   480

Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu
            485   490   495

Pro Ala Pro Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro
            500   505   510

Glu Thr Pro Pro Pro Thr Thr Ser Glu Val Ser Thr Pro Thr Thr Thr
        515   520   525

Lys Glu Pro Thr Thr Ile His Lys Ser Pro Asp Glu Ser Thr Pro Glu
        530   535   540

Leu Ser Ala Glu Pro Thr Pro Lys Ala Leu Glu Asn Ser Pro Lys Glu
545   550   555   560

Pro Gly Val Pro Thr Thr Lys Thr Pro Ala Ala Thr Lys Pro Glu Met
            565   570   575

Thr Thr Thr Ala Lys Asp Lys Thr Thr Glu Arg Asp Leu Arg Thr Thr
            580   585   590

Pro Glu Thr Thr Thr Ala Ala Pro Lys Met Thr Lys Glu Thr Ala Thr
        595   600   605

Thr Thr Glu Lys Thr Thr Glu Ser Lys Ile Thr Ala Thr Thr Thr Gln
        610   615   620

Val Thr Ser Thr Thr Thr Gln Asp Thr Thr Pro Phe Lys Ile Thr Thr
625   630   635   640

Leu Lys Thr Thr Thr Leu Ala Pro Lys Val Thr Thr Thr Lys Lys Thr
                 645   650   655

Ile Thr Thr Thr Glu Ile Met Asn Lys Pro Glu Glu Thr Ala Lys Pro
              660   665   670

Lys Asp Arg Ala Thr Asn Ser Lys Ala Thr Thr Pro Lys Pro Gln Lys
        675   680   685

Pro Thr Lys Ala Pro Lys Lys Pro Thr Ser Thr Lys Lys Pro Lys Thr
    690   695   700

Met Pro Arg Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg Lys Met
705   710   715   720

Thr Ser Thr Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala Glu Ala
             725   730   735

Met Leu Gln Thr Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser Lys Leu
            740   745   750

Val Glu Val Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu Gly Glu
       755   760   765

Thr Pro His Met Leu Leu Arg Pro His Val Phe Met Pro Glu Val Thr
    770   775   780

Pro Asp Met Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile Ile Ile
785   790   795   800

Asn Pro Met Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys Pro Val
             805   810   815

Asp Gly Leu Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe Arg Gly
            820   825   830

His Tyr Phe Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro Ala Arg
       835   840   845

Arg Ile Thr Glu Val Trp Gly Ile Pro Ser Pro Ile Asp Thr Val Phe
   850   855   860

Thr Arg Cys Asn Cys Glu Gly Lys Thr Phe Phe Phe Lys Asp Ser Gln
865   870   875   880

Tyr Trp Arg Phe Thr Asn Asp Ile Lys Asp Ala Gly Tyr Pro Lys Pro
            885   890   895

Ile Phe Lys Gly Phe Gly Gly Leu Thr Gly Gln Ile Val Ala Ala Leu
         900   905   910

Ser Thr Ala Lys Tyr Lys Asn Trp Pro Glu Ser Val Tyr Phe Phe Lys
       915   920   925

Arg Gly Gly Ser Ile Gln Gln Tyr Ile Tyr Lys Gln Glu Pro Val Gln

```
          930                    935                    940
```

Lys Cys Pro Gly Arg Arg Pro Ala Leu Asn Tyr Pro Val Tyr Gly Glu
945   950   955   960

Met Thr Gln Val Arg Arg Arg Arg Phe Glu Arg Ala Ile Gly Pro Ser
                965   970   975

Gln Thr His Thr Ile Arg Ile Gln Tyr Ser Pro Ala Arg Leu Ala Tyr
              980   985   990

Gln Asp Lys Gly Val Leu His Asn Glu Val Lys Val Ser Ile Leu Trp
         995   1000   1005

Arg Gly Leu Pro Asn Val Val Thr Ser Ala Ile Ser Leu Pro Asn
         1010   1015   1020

Ile Arg Lys Pro Asp Gly Tyr Asp Tyr Tyr Ala Phe Ser Lys Asp
         1025   1030   1035

Gln Tyr Tyr Asn Ile Asp Val Pro Ser Arg Thr Ala Arg Ala Ile
         1040   1045   1050

Thr Thr Arg Ser Gly Gln Thr Leu Ser Lys Val Trp Tyr Asn Cys
         1055   1060   1065

Pro

<210>   20
<211>   421
<212>   DNA
<213>   Artificial

<220>
<223>   Lub:4 DNA insert from cDNA cassette-1 and three synthetic cDNA
        cassette-2 sequences.

<400>   20
gcgcgcccac aactccaaaa gagcccgcac ctaccacgac aaagtcagct cctactacgc   60

ccaaagagcc agcgccgacg actactaaag aaccggcacc caccacgcct aaagaaccag   120

cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgcaccc acaacaccaa   180

aggagccggc ccctacgact cctaaagaac cagcccctac tacgacaaag gagcctgcac   240

ccacaaccac gaagagcgca cccacaacac caaaggagcc ggcccctacg actcctaaag   300

aaccagcccc tactacgaca aaggagcctg cacccacaac cacgaagagc gcacccacaa   360

caccaaagga gccggcccct acgactccta aggaacccaa accggcacca accactccgg   420

a   421
```

<210> 21
<211> 139
<212> PRT
<213> Artificial

<220>
<223> 139 amino acids encoded by Lub:4 DNA insert (12 KEPAPTT sequences between S373 and E513 in SEQ ID NO: 19)

<400> 21

```
Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
1               5                   10 ·                15

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
            20                  25                  30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
            35                  40                  45

Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro
    50                  55          ·       60

Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro
65                  70                  75                  80

Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
            85                  90                  95

Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro Thr
            100                 105                 110

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
            115                 120                 125

Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro
    130                 135
```

<210> 22
<211> 3303 ·
<212> DNA
<213> Artificial

<220>
<223> Recombinant PRG4-Lub:5 cDNA construct

<400> 22
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atggcatgga aaacacttcc catttacctg ttgttgctgc tgtctgtttt cgtgattcag     60

caagtttcat ctcaagattt atcaagctgt gcagggagat gtggggaagg gtattctaga     120

gatgccacct gcaactgtga ttataactgt caacactaca tggagtgctg ccctgatttc     180
```

```
aagagagtct gcactgcgga gctttcctgt aaaggccgct gctttgagtc cttcgagaga    240

gggagggagt gtgactgcga cgcccaatgt aagaagtatg acaagtgctg tcccgattat    300

gagagtttct gtgcagaagt gcataatccc acatcaccac catcttcaaa gaaagcacct    360

ccaccttcag gagcatctca aaccatcaaa tcaacaacca aacgttcacc caaaccacca    420

aacaagaaga agactaagaa agttatagaa tcagaggaaa taacagaaga acattctgtt    480

tctgaaaatc aagagcctc ctccagtagc agttcaagta gttcgtcgtc gacaatttgg    540

aaaatcaagt cttccaaaaa ttcagctgct aatagagaat tacagaagaa actcaaagta    600

aaagataaca agaagaacag aactaaaaag aaacctaccc ccaaaccacc agttgtagat    660

gaagctggaa gtggattgga caatggtgac ttcaaggtca caactcctga cacgtctacc    720

acccaacaca ataaagtcag cacatctccc aagatcacaa cagcaaaacc aataaatccc    780

agacccagtc ttccacctaa ttctgataca tctaaagaga cgtctttgac agtgaataaa    840

gagacaacag ttgaaactaa agaaactact acaacaaata aacagacttc aactgatgga    900

aaagagaaga ctacttccgc taaagagaca caaagtatag agaaaacatc tgctaaagat    960

ttagcaccca catctaaagt gctggctaaa cctacaccca aagctgaaac tacaaccaaa   1020

ggccctgctc tcaccactcc caaggagccc acgcccacca ctcccaagga gcctgcatct   1080

accacaccca aagagcccac acctaccacc atcaagagcg cgcccacaac tccaaaagag   1140

cccgcaccta ccacgacaaa gtcagctcct actacgccca aagagccagc gccgacgact   1200

actaaagaac cggcacccac cacgcctaaa gaaccagccc ctactacgac aaaggagcct   1260

gcacccacaa ccacgaagag cgcacccaca acaccaaagg agccggcccc tacgactcct   1320

aaagaaccag cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgcaccc   1380

acaacaccaa aggagccggc ccctacgact cctaaagaac cagcccctac tacgacaaag   1440

gagcctgcac ccacaaccac gaagagcgca cccacaacac caaaggagcc ggcccctacg   1500

actcctaaag aaccagcccc tactacgaca aaggagcctg cacccacaac cacgaagagc   1560

gcacccacaa caccaaagga gccggcccct acgactccta aggaacccaa accggcacca   1620

accactccgg aaacacctcc tccaaccact tcagaggtct ctactccaac taccaccaag   1680

gagcctacca ctatccacaa aagccctgat gaatcaactc ctgagctttc tgcagaaccc   1740

acaccaaaag ctcttgaaaa cagtcccaag gaacctggtg tacctacaac taagacgccg   1800
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```
gcggcgacta aacctgaaat gactacaaca gctaaagaca agacaacaga aagagactta    1860

cgtactacac ctgaaactac aactgctgca cctaagatga caaaagagac agcaactaca    1920

acagaaaaaa ctaccgaatc caaaataaca gctacaacca cacaagtaac atctaccaca    1980

actcaagata ccacaccatt caaaattact actcttaaaa caactactct tgcacccaaa    2040

gtaactacaa caaaaaagac aattactacc actgagatta tgaacaaacc tgaagaaaca    2100

gctaaaccaa aagacagagc tactaattct aaagcgacaa ctcctaaacc tcaaaagcca    2160

accaaagcac ccaaaaaacc cacttctacc aaaaagccaa aaacaatgcc tagagtgaga    2220

aaaccaaaga cgacaccaac tccccgcaag atgacatcaa caatgccaga attgaaccct    2280

acctcaagaa tagcagaagc catgctccaa accaccacca gacctaacca aactccaaac    2340

tccaaactag ttgaagtaaa tccaaagagt gaagatgcag gtggtgctga aggagaaaca    2400

cctcatatgc ttctcaggcc ccatgtgttc atgcctgaag ttactcccga catggattac    2460

ttaccgagag tacccaatca aggcattatc atcaatccca tgctttccga tgagaccaat    2520

atatgcaatg gtaagccagt agatggactg actactttgc gcaatgggac attagttgca    2580

ttccgaggtc attatttctg gatgctaagt ccattcagtc caccatctcc agctcgcaga    2640

attactgaag tttggggtat tccttccccc attgatactg tttttactag gtgcaactgt    2700

gaaggaaaaa ctttcttctt taaggattct cagtactggc gttttaccaa tgatataaaa    2760

gatgcagggt accccaaacc aattttcaaa ggatttggag gactaactgg acaaatagtg    2820

gcagcgcttt caacagctaa atataagaac tggcctgaat ctgtgtattt tttcaagaga    2880

ggtggcagca ttcagcagta tatttataaa caggaacctg tacagaagtg ccctggaaga    2940

aggcctgctc taaattatcc agtgtatgga gaaatgacac aggttaggag acgtcgcttt    3000

gaacgtgcta taggaccttc tcaaacacac accatcagaa ttcaatattc acctgccaga    3060

ctggcttatc aagacaaagg tgtccttcat aatgaagtta aagtgagtat actgtggaga    3120

ggacttccaa atgtggttac ctcagctata tcactgccca acatcagaaa acctgacggc    3180

tatgattact atgccttttc taaagatcaa tactataaca ttgatgtgcc tagtagaaca    3240

gcaagagcaa ttactactcg ttctgggcag accttatcca aagtctggta caactgtcct    3300

taa                                                                  3303
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<210>   23
<211>   1100

<212>   PRT
<213>   Artificial

<220>
<223>   Amino acid sequence of entire PRG4-LUB:5 protein.

<400>   23

Met Ala Trp Lys Thr Leu Pro Ile Tyr Leu Leu Leu Leu Leu Ser Val
1   5   10   15

Phe Val Ile Gln Gln Val Ser Ser Gln Asp Leu Ser Ser Cys Ala Gly
            20   25   30

Arg Cys Gly Glu Gly Tyr Ser Arg Asp Ala Thr Cys Asn Cys Asp Tyr
        35   40   45

Asn Cys Gln His Tyr Met Glu Cys Cys Pro Asp Phe Lys Arg Val Cys
    50   55   60

Thr Ala Glu Leu Ser Cys Lys Gly Arg Cys Phe Glu Ser Phe Glu Arg
65   70   75   80

Gly Arg Glu Cys Asp Cys Asp Ala Gln Cys Lys Lys Tyr Asp Lys Cys
            85   90   95

Cys Pro Asp Tyr Glu Ser Phe Cys Ala Glu Val His Asn Pro Thr Ser
        100   105   110

Pro Pro Ser Ser Lys Lys Ala Pro Pro Pro Ser Gly Ala Ser Gln Thr
        115   120   125

Ile Lys Ser Thr Thr Lys Arg Ser Pro Lys Pro Pro Asn Lys Lys Lys
    130   135   140

Thr Lys Lys Val Ile Glu Ser Glu Glu Ile Thr Glu Glu His Ser Val
145   150   155   160

Ser Glu Asn Gln Glu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
            165   170   175

Ser Thr Ile Trp Lys Ile Lys Ser Ser Lys Asn Ser Ala Ala Asn Arg
            180   185   190

Glu Leu Gln Lys Lys Leu Lys Val Lys Asp Asn Lys Lys Asn Arg Thr
        195   200   205

Lys Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu Ala Gly Ser
    210   215   220

Gly Leu Asp Asn Gly Asp Phe Lys Val Thr Thr Pro Asp Thr Ser Thr
225   230   235   240

Thr Gln His Asn Lys Val Ser Thr Ser Pro Lys Ile Thr Thr Ala Lys
            245   250   255

Pro Ile Asn Pro Arg Pro Ser Leu Pro Pro Asn Ser Asp Thr Ser Lys
          260   265   270

Glu Thr Ser Leu Thr Val Asn Lys Glu Thr Thr Val Glu Thr Lys Glu
      275   280   285

Thr Thr Thr Thr Asn Lys Gln Thr Ser Thr Asp Gly Lys Glu Lys Thr
    290   295   300

Thr Ser Ala Lys Glu Thr Gln Ser Ile Glu Lys Thr Ser Ala Lys Asp
305   310   315   320

Leu Ala Pro Thr Ser Lys Val Leu Ala Lys Pro Thr Pro Lys Ala Glu
          325   330   335

Thr Thr Thr Lys Gly Pro Ala Leu Thr Thr Pro Lys Glu Pro Thr Pro
          340   345   350

Thr Thr Pro Lys Glu Pro Ala Ser Thr Thr Pro Lys Glu Pro Thr Pro
      355   360   365

Thr Thr Ile Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
    370   375   380

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
385   390   395   400

Thr Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
          405   410   415

Thr Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro
          420   425   430

Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr
      435   440   445

Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys
    450   455   460

Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys
465   470   475   480

Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu
          485   490   495

Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu
          500   505   510

Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro
          515   520   525

Ala Pro Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro Glu
    530   535   540

Thr Pro Pro Pro Thr Thr Ser Glu Val Ser Thr Pro Thr Thr Thr Lys
545   550   555   560

Glu Pro Thr Thr Ile His Lys Ser Pro Asp Glu Ser Thr Pro Glu Leu
                565   570   575

Ser Ala Glu Pro Thr Pro Lys Ala Leu Glu Asn Ser Pro Lys Glu Pro
            580   585 .   590

Gly Val Pro Thr Thr Lys Thr Pro Ala Ala Thr Lys Pro Glu Met Thr
        595   600   605

Thr Thr Ala Lys Asp Lys Thr Thr Glu Arg Asp Leu Arg Thr Thr Pro
    610   615   620

Glu Thr Thr Thr Ala Ala Pro Lys Met Thr Lys Glu Thr Ala Thr Thr
625   630   635   640

Thr Glu Lys Thr Thr Glu Ser Lys Ile Thr Ala Thr Thr Thr Gln Val
            645   650   655

Thr Ser Thr Thr Thr Gln Asp Thr Thr Pro Phe Lys Ile Thr Thr Leu
        660   665   670

Lys Thr Thr Thr Leu Ala Pro Lys Val Thr Thr Thr Lys Lys Thr Ile
    675   680   685

Thr Thr Thr Glu Ile Met Asn Lys Pro Glu Glu Thr Ala Lys Pro Lys
    690   695   700

Asp Arg Ala Thr Asn Ser Lys Ala Thr Thr Pro Lys Pro Gln Lys Pro
705   710   715   720

Thr Lys Ala Pro Lys Lys Pro Thr Ser Thr Lys Lys Pro Lys Thr Met
            725   730   735

Pro Arg Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg Lys Met Thr
            740   745   750

Ser Thr Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala Glu Ala Met
            755   760   765

Leu Gln Thr Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser Lys Leu Val
    770   775   780

Glu Val Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu Gly Glu Thr
.785   790   795   800

Pro His Met Leu Leu Arg Pro His Val Phe Met Pro Glu Val Thr Pro
            805   810   815

Asp Met Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile Ile Ile Asn
            820   825   830

Pro Met Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys Pro Val Asp

```
        835                    840                    845

Gly Leu Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe Arg Gly His
    850                 855                 860

Tyr Phe Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro Ala Arg Arg
865                 870                 875                 880

Ile Thr Glu Val Trp Gly Ile Pro Ser Pro Ile Asp Thr Val Phe Thr
                885                 890                 895

Arg Cys Asn Cys Glu Gly Lys Thr Phe Phe Phe Lys Asp Ser Gln Tyr
            900                 905                 910

Trp Arg Phe Thr Asn Asp Ile Lys Asp Ala Gly Tyr Pro Lys Pro Ile
        915                 920                 925

Phe Lys Gly Phe Gly Gly Leu Thr Gly Gln Ile Val Ala Ala Leu Ser
    930                 935                 940

Thr Ala Lys Tyr Lys Asn Trp Pro Glu Ser Val Tyr Phe Phe Lys Arg
945                 950                 955                 960

Gly Gly Ser Ile Gln Gln Tyr Ile Tyr Lys Gln Glu Pro Val Gln Lys
            965                 970                 975

Cys Pro Gly Arg Arg Pro Ala Leu Asn Tyr Pro Val Tyr Gly Glu Met
        980                 985                 990

Thr Gln Val Arg Arg Arg Arg Phe Glu Arg Ala Ile Gly Pro Ser Gln
        995                 1000                1005

Thr His Thr Ile Arg Ile Gln Tyr Ser Pro Ala Arg Leu Ala Tyr
    1010                1015                1020

Gln Asp Lys Gly Val Leu His Asn Glu Val Lys Val Ser Ile Leu
    1025                1030                1035

Trp Arg Gly Leu Pro Asn Val Val Thr Ser Ala Ile Ser Leu Pro
    1040                1045                1050

Asn Ile Arg Lys Pro Asp Gly Tyr Asp Tyr Tyr Ala Phe Ser Lys
    1055                1060                1065

Asp Gln Tyr Tyr Asn Ile Asp Val Pro Ser Arg Thr Ala Arg Ala
    1070                1075                1080

Ile Thr Thr Arg Ser Gly Gln Thr Leu Ser Lys Val Trp Tyr Asn
    1085                1090                1095

Cys Pro
    1100
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<210> 24

<211> 514
<212> DNA
<213> Artificial

<220>
<223> Lub:5 DNA insert from cDNA cassette-1 and four synthetic cDNA
      cassette-2 sequences

<400> 24
gcgcgcccac aactccaaaa gagcccgcac ctaccacgac aaagtcagct cctactacgc   60

ccaaagagcc agcgccgacg actactaaag aaccggcacc caccacgcct aaagaaccag   120

cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgcaccc acaacaccaa   180

aggagccggc ccctacgact cctaaagaac cagccccctac tacgacaaag gagcctgcac   240

ccacaaccac gaagagcgca cccacaacac caaaggagcc ggcccctacg actcctaaag   300

aaccagcccc tactacgaca aaggagcctg cacccacaac cacgaagagc gcacccacaa   360

caccaaagga gccggcccct acgactccta agaaccagc ccctactacg acaaaggagc   420

ctgcacccac aaccacgaag agcgcaccca acaccaaa ggagccggcc cctacgactc   480

ctaaggaacc caaaccggca ccaaccactc cgga   514

<210> 25
<211> 170
<212> PRT
<213> Artificial

<220>
<223> 170 amino acids encoded by Lub:5 DNA insert (15 KEPAPTT sequences
      between S373 and E544 in SEQ ID NO: 23)

<400> 25

Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
1   5   10   15

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
            20   25   30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
        35   40   45

Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro
    50   55   60

Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro
65   70   75   80

Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr

```
                  85                      90                      95
Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro Thr
            100                     105                     110

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
            115                     120                     125

Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro Thr Thr
     130                     135                     140

Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Pro
145                     150                     155                     160

Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro
                165                     170
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<210> 26
<211> 45
<212> PRT
<213> Artificial

<220>
<223> amino acid sequence "APTTPKEPAPTTTKSAPTTPKEPAPTTT
      KEPAPTTPKEPAPTTTK" (45 amino acids) in preferred PRG4-LUB:N
      protein

<400> 26

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Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
1                   5                   10                  15

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
            20                  25                  30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys
            35                  40                  45
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<210> 27
<211> 31
<212> PRT
<213> Artificial

<220>
<223> amino acid sequence "KEPAPTTTKEPAPTTTKSAPTTPKEPAPTTP" (31 amino
      acids) repeated N-1 times in preferred PRG4-LUB:N protein

<400> 27

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Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro Thr Thr Thr
1                   5                   10                  15

Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Pro
```

20   25   30

```
<210>  28
<211>  22
<212>  PRT
<213>  Artificial

<220>
<223>  Amino acid sequence "EPAPTTTKSAPTTPKEPAPTTP" (22 amino acids)
       joining SEQ ID NO: 26 to (N-2) repeats of SEQ ID NO: 27 in
       preferred PRG4-LUB:N protein where N = 3 or more.

<400>  28

Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu
1               5                   10                  15

Pro Ala Pro Thr Thr Pro
            20


<210>  29
<211>  10
<212>  PRT
<213>  Artificial

<220>
<223>  Amino acid sequence "KEPKPAPTTP" (10 amino acids) in preferred
       PRG4-LUB:N protein where N = 2 or more.

<400>  29

Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro
1               5                   10
```